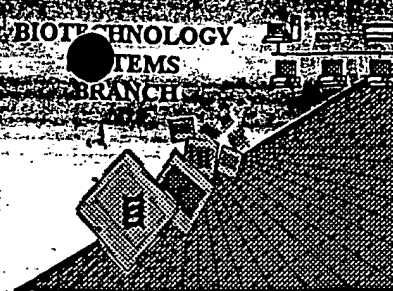


## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/981,206

Source: OIPE

Date Processed by STIC: 11/2/01

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## Raw Sequence Listing Error Summary

### ERROR DETECTED      SUGGESTED CORRECTION

SERIAL NUMBER: 09/981,206

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos      was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
     prevent "wrapping."
  
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering      use space characters, instead.
  
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
     ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
     each n or Xaa can only represent a single residue. Please present the maximum number of each  
     residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"      sequences(s)     . Normally, PatentIn would automatically generate this section from the  
     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
     the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
     Artificial or Unknown sequences.
  
- 7      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     This sequence is intentionally skipped  
  
     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)      <210> sequence id number  
     <400> sequence id number  
     000
  
- 9      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)      Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10 ✓ Invalid <213>      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response      scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
     is Artificial Sequence
  
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
     "Unknown." Please explain source of genetic material in <220> to <223> section.  
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"      resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/981,206

DATE: 11/02/2001

TIME: 15:26:24

Input Set : A:\es.txt

Output Set: N:\CRF3\11022001\I981206.raw

Does Not Comply  
Corrected Diskette Needed  
Errors on pp. 1-3

3 <110> APPLICANT: Achilefu, Samuel I.  
4 Rajagopalan, Raghavan  
5 Dorshow, Richard B.  
6 Bugaj, Joseph E.  
8 Mallinckrodt Inc.  
10 <120> TITLE OF INVENTION: Carbocyanine Dyes For Tandem, Photodiagnostic  
11 and Therapeutic Applications  
13 <130> FILE REFERENCE: MRD-74  
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/981,206  
16 <141> CURRENT FILING DATE: 2001-10-17  
W--> 18 <150> PRIOR APPLICATION NUMBER:  
W--> 19 <151> PRIOR FILING DATE: Do not respond if no other prior application include  
21 <160> NUMBER OF SEQ ID NOS: 8  
23 <170> SOFTWARE: PatentIn Version 3.1  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 8  
27 <212> TYPE: PRT  
28 <213> ORGANISM: Artificial Sequence  
30 <220> FEATURE:  
W--> 31 <221> NAME/KEY: MOD RES → put underscore between MOD + RES → MOD\_RES  
32 <222> LOCATION: (1)...(8)  
33 <223> OTHER INFORMATION: Xaa at location 1 represents D-Phe. Artificial sequence is  
34 completely synthesized.  
35 <223> OTHER INFORMATION: Xaa at locations 2 and 7 represents Cys with an  
36 intramolecular disulfide bond between two Cys  
37 amino acids. Artificial sequence is completely synthesized.  
38 <223> OTHER INFORMATION: Xaa at location 4 represents D-Trp. Artificial sequence is  
39 completely synthesized.  
41 <400> SEQUENCE: 1  
W--> 42 Xaa Xaa Tyr Xaa Lys Thr Xaa Thr  
43 1 5  
47 <210> SEQ ID NO: 2  
48 <211> LENGTH: 8  
49 <212> TYPE: PRT  
50 <213> ORGANISM: Artificial Sequence  
52 <220> FEATURE:  
W--> 53 <221> NAME/KEY: MOD RES  
54 <222> LOCATION: (1)...(8)  
55 <223> OTHER INFORMATION: Xaa at location 1 represents D-Phe. Artificial sequence is  
56 completely synthesized.  
57 <223> OTHER INFORMATION: Xaa at locations 2 and 7 represents Cys with an  
58 intramolecular disulfide bond between two Cys  
59 amino acids. Artificial sequence is completely synthesized.  
61 <223> OTHER INFORMATION: Xaa at location 4 represents D-Trp. Artificial sequence is  
62 completely synthesized.  
63 <223> OTHER INFORMATION: Xaa at location 8 represents Thr-OH. Artificial sequence is  
64 completely synthesized.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/981,206

DATE: 11/02/2001

TIME: 15:26:24

Input Set : A:\es.txt

Output Set: N:\CRF3\11022001\I981206.raw

66 <400> SEQUENCE: 2  
W--> 67 Xaa Xaa Tyr Xaa Lys Thr Xaa Xaa  
68 1 5  
71 <210> SEQ ID NO: 3  
72 <211> LENGTH: 11  
73 <212> TYPE: PRT  
74 <213> ORGANISM: Peptide - invalid; see error summary sheet, item 10  
76 <400> SEQUENCE: 3  
77 Gly Ser Gly Gln Trp Ala Val Gly His Leu Met  
78 1 5 10  
81 <210> SEQ ID NO: 4  
82 <211> LENGTH: 11  
83 <212> TYPE: PRT  
84 <213> ORGANISM: Peptide - same  
86 <400> SEQUENCE: 4  
87 Gly Asp Gly Gln Trp Ala Val Gly His Leu Met  
88 1 5 10  
92 <210> SEQ ID NO: 5  
93 <211> LENGTH: 8  
94 <212> TYPE: PRT  
95 <213> ORGANISM: Peptide - same  
97 <400> SEQUENCE: 5  
98 Asp Tyr Met Gly Trp Met Asp Phe  
99 1 5  
102 <210> SEQ ID NO: 6  
103 <211> LENGTH: 8  
104 <212> TYPE: PRT  
105 <213> ORGANISM: Artificial Sequence  
107 <220> FEATURE:  
W--> 108 <221> NAME/KEY: MOD RES  
109 <222> LOCATION: (1)...(8)  
110 <223> OTHER INFORMATION: Xaa at locations 3 and 6 represents Norleucine. Artificial  
111 sequence is completely synthesized.  
113 <400> SEQUENCE: 6  
W--> 114 Asp Tyr Xaa Gly Trp Xaa Asp Phe  
115 1 5  
118 <210> SEQ ID NO: 7  
119 <211> LENGTH: 8  
120 <212> TYPE: PRT  
121 <213> ORGANISM: Artificial Sequence  
123 <220> FEATURE:  
W--> 124 <221> NAME/KEY: MOD RES  
125 <222> LOCATION: (1)...(8)  
126 <223> OTHER INFORMATION: Xaa at location 1 represents D-Asp. Artificial sequence is  
127 completely synthesized.  
128 <223> OTHER INFORMATION: Xaa at locations 3 and 6 represents Norleucine. Artificial  
129 sequence is completely synthesized.  
131 <400> SEQUENCE: 7  
W--> 132 Xaa Tyr Xaa Gly Trp Xaa Asp Phe

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/981,206

DATE: 11/02/2001

TIME: 15:26:24

Input Set : A:\es.txt

Output Set: N:\CRF3\11022001\I981206.raw

133 1 5  
137 <210> SEQ ID NO: 8  
138 <211> LENGTH: 8  
139 <212> TYPE: PRT  
140 <213> ORGANISM: Artificial Sequence  
142 <220> FEATURE:  
W--> 143 <221> NAME/KEY: MOD RES  
144 <222> LOCATION: (1)...(8)  
145 <223> OTHER INFORMATION: Xaa at location 1 represents D-Lys. Artificial sequence is  
146 completely synthesized.  
148 <400> SEQUENCE: 8  
W--> 149 Xaa Pro Arg Arg Pro Tyr Ile Leu  
150 1 5

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/981,206

DATE: 11/02/2001

TIME: 15:26:25

Input Set : A:\es.txt

Output Set: N:\CRF3\11022001\I981206.raw

L:15 M:270 C: Current Application Number differs, Replaced Application Number  
L:18 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:  
L:19 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:31 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:53 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2  
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:108 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:124 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:143 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8